17-Assessment and characterization of the genetic diversity of viruses infecting cultivated yams (*Dioscorea* spp.) in Haïti

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Several viral species are known to infect yams (*Dioscorea* spp.) and to generate important yield losses on this vegetative propagated crop. Within the framework of the DEVAG project (Caribbean network for the development of agroecological horticultural systems) funded by the INTERREG IV Caribbean program, the inventory, the characterization and the prevalence of viruses infecting yams in Haïti have been undertaken to assess their impact on culture and to suggest appropriate control methods.

Approximately four hundred samples belonging to five yam species cultivated in Haïti (*D. alata*, *D. bulbifera*, *D. cayenensis*, *D. rotundata*, *D. trifida*) were collected in 2009 in farmers' fields in the five growing regions of yam. Virus detection was performed using broad spectrum PCR and RT-PCR tests targeting badnaviruses, CMV (genus *Cucumovirus*), potexviruses and potyviruses, after direct binding of viral particles on PCR tubes. Ninety four samples were infected by at least one of those viruses. The *Badnavirus* genus represents the most prevalent viral type. Hence, badnavirus RnaseH gene fragment (528 bp) was detected and amplified from most of the *D. bulbifera* samples (15/18) and *D. trifida* samples (6/6), and in half of the *D. alata* samples (61/132). Genetic diversity of these sequences is high (50-97%) and these sequences belong to six out of thirteen groups of yam badnaviruses identified by Kenyon *et al.* (2008). Analysis of the potyvirus sequences (CP - 282 bp) obtained from ten samples revealed the existence of YMMV on *D. alata* (7/132) and *D. trifida* (1/6) samples. Similarly, two strains of a new potyvirus were found in *D. trifida* samples (2/6) with a nucleotide identity of 74-79% with two viral species, ALiMV and PTV. Furthermore, three sequences (245 bp) related to the RdRp gene of potexviruses, with 71-78% of nucleotide identity with PAMV and PepMV were found in two *D. bulbifera* and *D. rotundata* plants.
This is the first inventory of yam viruses in Haïti which highlights a high viral prevalence rate with large amount of diversity within each virus species tested. Excepted for badnaviruses for which impact on yam production is misunderstood, the pressure of RNA viruses appears to be very low for the most common varieties, but strong for the rarer cultivars suggesting that a dramatic varietal genetic erosion is underway.

Kenyon L., Lebas B.S.M., Seal S.E. (2008). Yams (*Dioscorea* spp.) from the South Pacific Islands contain many novel badnaviruses: implications for international movement of yam germplasm. *Archives of Virology* 153: 877-889.

Mots-clés:
Epidemiology, Badnavirus, Potexvirus, Potyvirus